



PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/018,192

DATE: 11/18/2002

TIME: 15:14:35

Input Set : A:\EP.txt

Output Set: N:\CRF4\11182002\J018192.raw

W--> 1 Dkt. 1795/59138-B-PCT-US/JPW/PL *delete*

5 <110> APPLICANT: Synaptic Pharmaceutical Corporation

7 <120> TITLE OF INVENTION: DNA Encoding SNORF36a and SNORF36b Receptors

9 <130> FILE REFERENCE: 59138-B-PCT/JPW

C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/018,192

C--> 12 <141> CURRENT FILING DATE: 2002-11-01

14 <150> PRIOR APPLICATION NUMBER: 09/518,914

15 <151> PRIOR FILING DATE: 2000-03-03

17 <150> PRIOR APPLICATION NUMBER: 09/303,593

18 <151> PRIOR FILING DATE: 1999-05-03

20 <160> NUMBER OF SEQ ID NOS: 48

22 <170> SOFTWARE: PatentIn Ver. 2.1

24 <210> SEQ ID NO: 1

25 <211> LENGTH: 1508

26 <212> TYPE: DNA

27 <213> ORGANISM: Homo sapiens

29 <400> SEQUENCE: 1

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32 agcctggggc ggttcccatc catcagtcct acagcacctg ggacttgggc tgcctgcctg 180
33 gtccccctcc ccacgggtga tgttccagac catgcccact ataccctggg cacagtgatc 240
34 ttgctggtgg gactcacggg gatgctgggc aacctgacgg tcatctatac cttctgcagg 300
35 agcagaagcc tccggacacc tgccaacatg ttcattatca acctcgcggt cagcgacttc 360
36 ctcatgtcct tcacccaggc ccctgtcttc ttcaccagta gcctctataa gcagtggctc 420
37 tttggggaga caggctgcga gttctatgcc ttctgtggag ctctctttgg catttcctcc 480
38 atgatcacc tgaaggccat cgccctggac cgtacctgg taatcacacg cccgctggcc 540
39 acctttggtg tggcgtccaa gaggcgtgog gcatttgtcc tgctgggcgt ttggctctat 600
40 gccctggcct ggagtctgcc acccttcttc ggctggagcg cctacgtgcc cgaggggttg 660
41 ctgacatcct gctcctggga ctacatgagc ttcacgccgg ccgtgcgtgc ctacaccatg 720
42 cttctctgct gcttcgtgtt cttcctccct ctgcttatca tcatctactg ctacatcttc 780
43 atcttcaggg ccatccggga gacaggacgg gctctccaga ccttcggggc ctgcaagggc 840
44 aatggcgagt ccctgtggca gcgcagcgg ctgcagagcg agtgcaagat ggccaagatc 900
45 atgctgctgg tcatectcct cttcgtgctc tcttgggctc cctattccgc tgtggccctg 960
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50 aggggtggca ttgccagca cctgccctgc ctgggggtgc tgctgggtgt atcacgccg 1140
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52 tccaacctca gctggatctc catacggagg cgccaggagt ccctgggctc ggagagttag 1260
53 gtgggctgga cacacatgga ggcagcagct gtgtggggag ctgccagca agcaaattgg 1320
54 cggtcctctt acggtcaggg tctggaggac ttggaagcca aggcaccccc cagaccccag 1380
55 ggacacgaag cagagactcc agggaagacc aaggggctga tccccagcca ggaccccagg 1440
56 atgtaggacg cccactggct ctccctttct tctgagacac atccagcccc cccacgtctc 1500
57 cctcatat
1508

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Hand

Does Not Comply
Corrected Diskette Needed

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62 <212> TYPE: PRT
63 <213> ORGANISM: Homo sapiens
64 <400> SEQUENCE: 2
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69 Pro Ser Cys Met Ala Thr Pro Ala Pro Pro Ser Trp Trp Asp Ser Ser
70          20          25          30
72 Gln Ser Ser Ile Ser Ser Leu Gly Arg Leu Pro Ser Ile Ser Pro Thr
73          35          40          45
75 Ala Pro Gly Thr Trp Ala Ala Ala Trp Val Pro Leu Pro Thr Val Asp
76          50          55          60
78 Val Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile Leu Leu Val
79  65          70          75          80
81 Gly Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr Thr Phe Cys
82          85          90          95
84 Arg Ser Arg Ser Leu Arg Thr Pro Ala Asn Met Phe Ile Ile Asn Leu
85          100         105         110
87 Ala Val Ser Asp Phe Leu Met Ser Phe Thr Gln Ala Pro Val Phe Phe
88          115         120         125
90 Thr Ser Ser Leu Tyr Lys Gln Trp Leu Phe Gly Glu Thr Gly Cys Glu
91          130         135         140
93 Phe Tyr Ala Phe Cys Gly Ala Leu Phe Gly Ile Ser Ser Met Ile Thr
94 145          150         155         160
96 Leu Thr Ala Ile Ala Leu Asp Arg Tyr Leu Val Ile Thr Arg Pro Leu
99          165         170         175
101 Ala Thr Phe Gly Val Ala Ser Lys Arg Arg Ala Ala Phe Val Leu Leu
102          180         185         190
104 Gly Val Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro Phe Phe Gly
105          195         200         205
107 Trp Ser Ala Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys Ser Trp Asp
108          210         215         220
110 Tyr Met Ser Phe Thr Pro Ala Val Arg Ala Tyr Thr Met Leu Leu Cys
111 225          230         235         240
113 Cys Phe Val Phe Phe Leu Pro Leu Leu Ile Ile Ile Tyr Cys Tyr Ile
114          245         250         255
116 Phe Ile Phe Arg Ala Ile Arg Glu Thr Gly Arg Ala Leu Gln Thr Phe
117          260         265         270
119 Gly Ala Cys Lys Gly Asn Gly Glu Ser Leu Trp Gln Arg Gln Arg Leu
120          275         280         285
122 Gln Ser Glu Cys Lys Met Ala Lys Ile Met Leu Leu Val Ile Leu Leu
123          290         295         300
125 Phe Val Leu Ser Trp Ala Pro Tyr Ser Ala Val Ala Leu Val Ala Phe
126 305          310         315         320
128 Ala Gly Tyr Ala His Val Leu Thr Pro Tyr Met Ser Ser Val Pro Ala
129          325         330         335
131 Val Ile Ala Lys Ala Ser Ala Ile His Asn Pro Ile Ile Tyr Ala Ile
132          340         345         350

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134 Thr His Pro Lys Tyr Arg Val Ala Ile Ala Gln His Leu Pro Cys Leu
135          355          360          365
137 Gly Val Leu Leu Gly Val Ser Arg Arg His Ser Arg Pro Tyr Pro Ser
138          370          375          380
140 Tyr Arg Ser Thr His Arg Ser Thr Leu Thr Ser His Thr Ser Asn Leu
141 385          390          395          400
143 Ser Trp Ile Ser Ile Arg Arg Arg Gln Glu Ser Leu Gly Ser Glu Ser
144          405          410          415
147 Glu Val Gly Trp Thr His Met Glu Ala Ala Ala Val Trp Gly Ala Ala
148          420          425          430
150 Gln Gln Ala Asn Gly Arg Ser Leu Tyr Gly Gln Gly Leu Glu Asp Leu
151          435          440          445
153 Glu Ala Lys Ala Pro Pro Arg Pro Gln Gly His Glu Ala Glu Thr Pro
154          450          455          460
156 Gly Lys Thr Lys Gly Leu Ile Pro Ser Gln Asp Pro Arg Met
157 465          470          475
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161 <211> LENGTH: 1541
162 <212> TYPE: DNA
163 <213> ORGANISM: Homo sapiens
165 <400> SEQUENCE: 3
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167 agctgcatgg ccaccccagc accaccacgc tgggtggaca gctcccagag cagcatctcc 120
168 agcctgggccc ggcttccatc catcagtccc acagcacctg ggacttgggc tgctgcctgg 180
169 gtccccctcc ccacggttga tgttcagac catgccact ataccctggg cacagtgatc 240
170 ttgctggtgg gactcacggg gatgctgggc aacctgacgg tcatctatac cttctgcaga 300
171 gctgtgcttc gtggagtcac tgtgatgatg cagagcagaa gcctccggac acctgccaac 360
172 atgttcatta tcaacctcgc ggtcagcgac ttcctcatgt ccttcaccca ggcccctgtc 420
173 ttcttcacca gtagcctcta taagcagtgg ctctttgggg agacaggctg cgagttctat 480
174 gccttctgtg gagctctctt tggcatttcc tccatgatca ccctgacggc catcgccctg 540
175 gaccgctacc tggtaatcac acgcccgtg gccaccttg gtgtggcgtc caagaggcgt 600
176 gcggcatttg tcctgctggg cgtttggctc tatgccctgg cctggagtct gccacccttc 660
177 ttcggctgga gcgcctacgt gcccgagggg ttgctgacat cctgctcctg ggactacatg 720
178 agcttcacgc cggccgtgcg tgcctacacc atgcttctct gctgcttcgt gttcttcttc 780
179 cctctgctta tcatcatcta ctgctacatc ttcatttca gggccatccg ggagacagga 840
180 cgggctctcc agaccttcgg ggctgcaag ggcaatggcg agtccctgtg gcagcggcag 900
181 cggctgcaga gcgagtgcaa gatggccaag atcatgctgc tggtcaccc cctcttcgtg 960
182 ctctcctggg ctccctattc cgctgtggcc ctggtggcct ttgctgggta cgcacacgtc 1020
183 ctgacaccct acatgagctc ggtgccagcc gtcacgccca aggcctctgc aatccacaac 1080
184 cccatcattt acgccatcac ccaccccaag tacagggtgg ccattgccc gcacctgccc 1140
185 tgccctgggg tgctgctggg tgtatcacgc cggcacagtc gcccctaccc cagctaccgc 1200
186 tccacccacc gctccacgct gaccagccac acctccaacc tcagctggat ctccatacgg 1260
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188 gctgtgtggg gagctgcccc gcaagcaaat gggcggtccc tctacggtea gggctcggag 1380
189 gacttggaag ccaaggcacc cccagacccc cagggacacg aagcagagac tccagggaag 1440
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191 tcttctgaga cacatccagc ccccccacgt ctccctcata t 1541
195 <210> SEQ ID NO: 4
196 <211> LENGTH: 489

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197 <212> TYPE: PRT
198 <213> ORGANISM: Homo sapiens
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204 Pro Ser Cys Met Ala Thr Pro Ala Pro Pro Ser Trp Trp Asp Ser Ser
205 20 25 30
207 Gln Ser Ser Ile Ser Ser Leu Gly Arg Leu Pro Ser Ile Ser Pro Thr
208 35 40 45
210 Ala Pro Gly Thr Trp Ala Ala Ala Trp Val Pro Leu Pro Thr Val Asp
211 50 55 60
213 Val Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile Leu Leu Val
214 65 70 75 80
216 Gly Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr Thr Phe Cys
217 85 90 95
219 Arg Ala Val Leu Arg Gly Val Thr Val Met Met Gln Ser Arg Ser Leu
220 100 105 110
222 Arg Thr Pro Ala Asn Met Phe Ile Ile Asn Leu Ala Val Ser Asp Phe
223 115 120 125
225 Leu Met Ser Phe Thr Gln Ala Pro Val Phe Phe Thr Ser Ser Leu Tyr
226 130 135 140
228 Lys Gln Trp Leu Phe Gly Glu Thr Gly Cys Glu Phe Tyr Ala Phe Cys
229 145 150 155 160
231 Gly Ala Leu Phe Gly Ile Ser Ser Met Ile Thr Leu Thr Ala Ile Ala
232 165 170 175
234 Leu Asp Arg Tyr Leu Val Ile Thr Arg Pro Leu Ala Thr Phe Gly Val
235 180 185 190
237 Ala Ser Lys Arg Arg Ala Ala Phe Val Leu Leu Gly Val Trp Leu Tyr
238 195 200 205
240 Ala Leu Ala Trp Ser Leu Pro Pro Phe Phe Gly Trp Ser Ala Tyr Val
243 210 215 220
245 Pro Glu Gly Leu Leu Thr Ser Cys Ser Trp Asp Tyr Met Ser Phe Thr
246 225 230 235 240
248 Pro Ala Val Arg Ala Tyr Thr Met Leu Leu Cys Cys Phe Val Phe Phe
249 245 250 255
251 Leu Pro Leu Leu Ile Ile Ile Tyr Cys Tyr Ile Phe Ile Phe Arg Ala
252 260 265 270
254 Ile Arg Glu Thr Gly Arg Ala Leu Gln Thr Phe Gly Ala Cys Lys Gly
255 275 280 285
257 Asn Gly Glu Ser Leu Trp Gln Arg Gln Arg Leu Gln Ser Glu Cys Lys
258 290 295 300
260 Met Ala Lys Ile Met Leu Leu Val Ile Leu Leu Phe Val Leu Ser Trp
261 305 310 315 320
263 Ala Pro Tyr Ser Ala Val Ala Leu Val Ala Phe Ala Gly Tyr Ala His
264 325 330 335
266 Val Leu Thr Pro Tyr Met Ser Ser Val Pro Ala Val Ile Ala Lys Ala
267 340 345 350
269 Ser Ala Ile His Asn Pro Ile Ile Tyr Ala Ile Thr His Pro Lys Tyr
270 355 360 365

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272 Arg Val Ala Ile Ala Gln His Leu Pro Cys Leu Gly Val Leu Leu Gly
273      370                      375                      380
275 Val Ser Arg Arg His Ser Arg Pro Tyr Pro Ser Tyr Arg Ser Thr His
276 385                      390                      395                      400
278 Arg Ser Thr Leu Thr Ser His Thr Ser Asn Leu Ser Trp Ile Ser Ile
279                      405                      410                      415
281 Arg Arg Arg Gln Glu Ser Leu Gly Ser Glu Ser Glu Val Gly Trp Thr
282                      420                      425                      430
284 His Met Glu Ala Ala Ala Val Trp Gly Ala Ala Gln Gln Ala Asn Gly
285                      435                      440                      445
287 Arg Ser Leu Tyr Gly Gln Gly Leu Glu Asp Leu Glu Ala Lys Ala Pro
288                      450                      455                      460
291 Pro Arg Pro Gln Gly His Glu Ala Glu Thr Pro Gly Lys Thr Lys Gly
292 465                      470                      475                      480
294 Leu Ile Pro Ser Gln Asp Pro Arg Met
295                      485
298 <210> SEQ ID NO: 5
299 <211> LENGTH: 250
300 <212> TYPE: DNA
301 <213> ORGANISM: Rattus norvegicus
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305 caagagacgg acggcactag tcttgctagg tgtctggctc tatgccctgg cctggagtct 120
306 gccgcctttc ttggctgga gcgcctacgt gcccgagggg ctgctgacat cctgctcctg 180
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308 cttcttcctc                                     250
311 <210> SEQ ID NO: 6
312 <211> LENGTH: 83
313 <212> TYPE: PRT
314 <213> ORGANISM: Rattus norvegicus
316 <400> SEQUENCE: 6
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320 Gly Met Arg Ser Lys Arg Arg Thr Ala Leu Val Leu Leu Gly Val Trp
321                      20                      25                      30
323 Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro Phe Phe Gly Trp Ser Ala
324                      35                      40                      45
326 Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys Ser Trp Asp Tyr Val Thr
327 50                      55                      60
329 Phe Thr Pro Leu Val Arg Ala Tyr Thr Met Leu Leu Phe Cys Phe Val
330 65                      70                      75                      80
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339 <211> LENGTH: 1473
340 <212> TYPE: DNA
341 <213> ORGANISM: Rattus norvegicus
343 <400> SEQUENCE: 7
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/018,192

DATE: 11/18/2002

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Output Set: N:\CRF4\11182002\J018192.raw

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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date